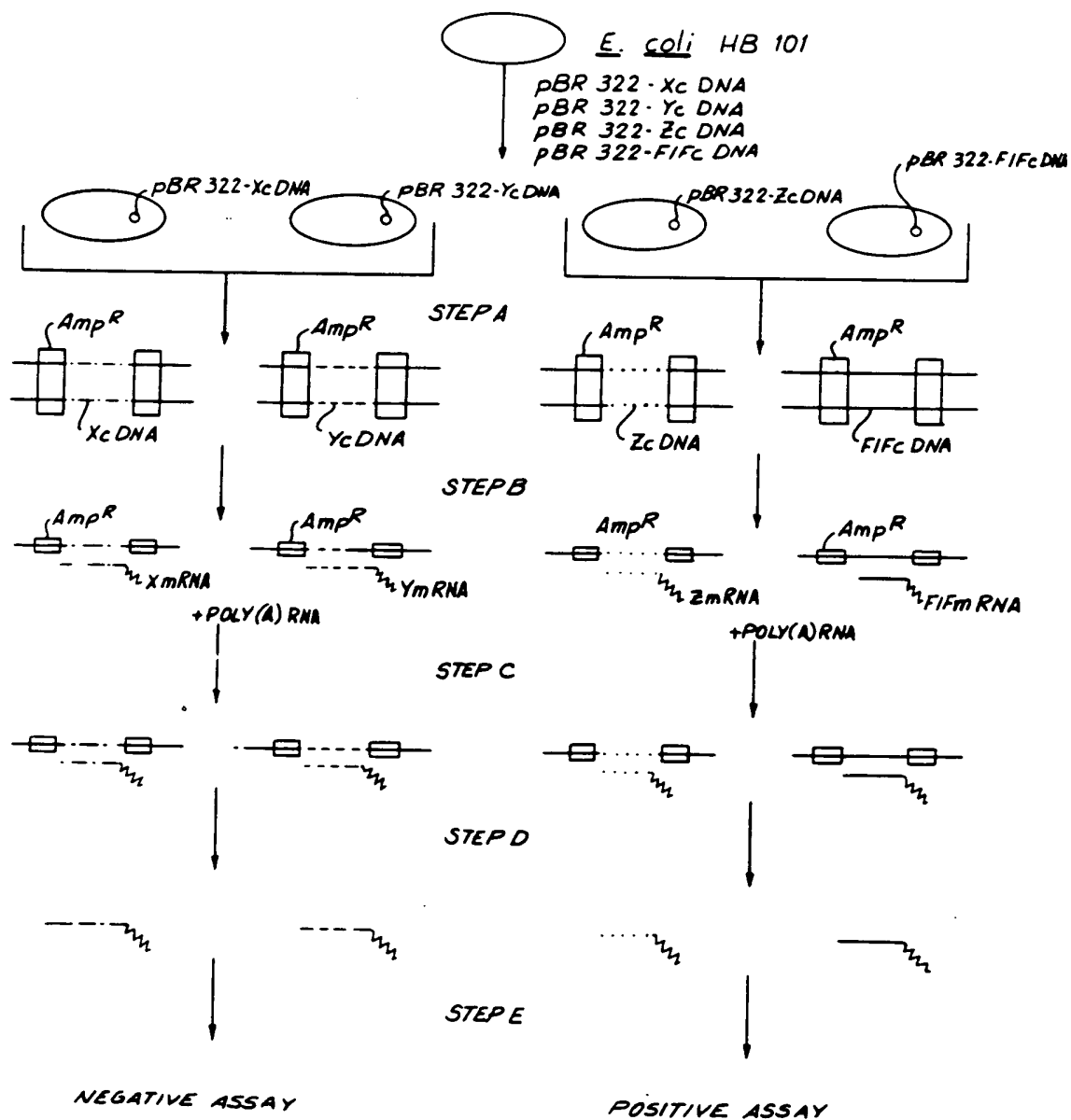
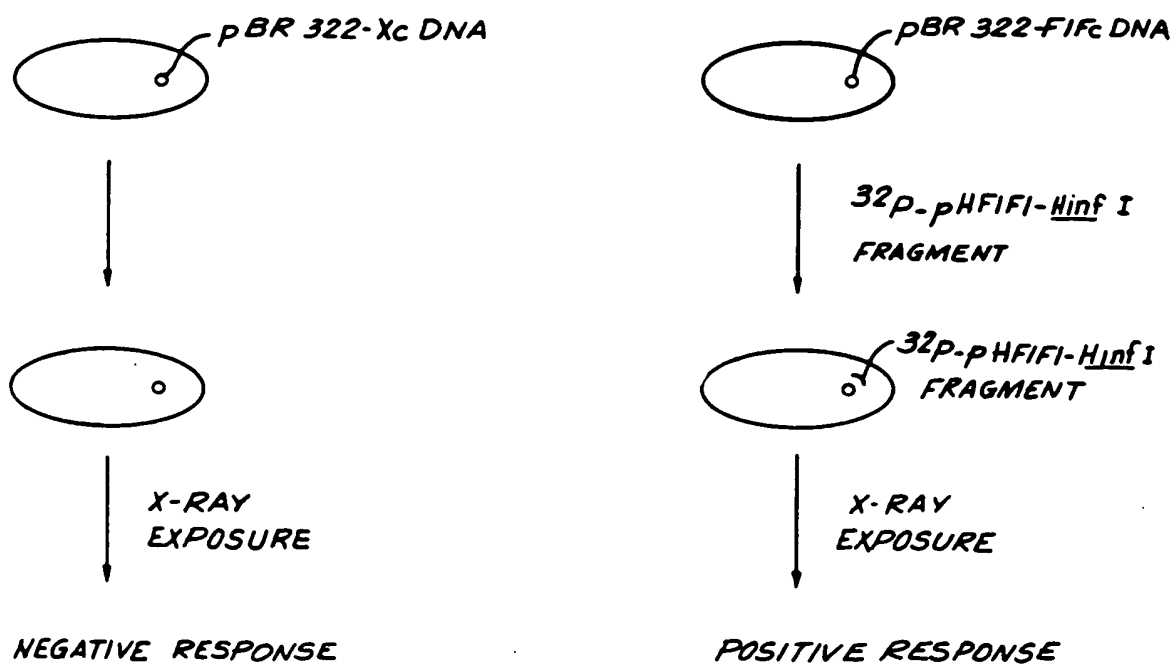




FIG. 2



**FIG. 3**



<sup>-10</sup>  
 MET-THR-ASN-LYS-CYS-LEU-LEU-GLN-ILE-ALA-LEU-LEU-  
<sup>-20</sup>  
 GCAA CCTTTCGAAG CCTTTGCTC GGCACAACAG GTAGTAGGCG ACACGTGTCG TGTGTTGAC ATG,ACC,AAC,AAG,TGT,CTC,CTC,CAA,ATT,GCT,CTC,CTG,100  
<sup>10</sup>      <sup>20</sup>  
 LEU-CYS-PHE-SER-THR-ALA-LEU-SER-MET-SER-TYR-ASN-LEU-LEU-GLY-PHE-LEU-GLN-ARG-SER-SER-ASN-PHE-GLN-CYS-GLN-LYS-LEU-LEU-  
<sup>-1</sup>      <sup>+1</sup>  
 TTG,TGC,TTT,CTC,ACT,ACA,GCT,CTT,TCG,ATG,AGC,TAC,AAC,TTG,CTT,GGA,TTT,CTA,CAA,AGA,AGC,AGC,AAT,TTT,CAG,TGT,CAG,AAG,CTC,CTG,190  
<sup>30</sup>      <sup>40</sup>      <sup>50</sup>  
 TRP-GLN-LEU-ASN-GLY-ARG-LEU-GLU-TYR-CYS-LEU-LYS-ASP-MET-ASN-PHE-ASP-ILE-PRO-GLU-GLU-ILE-LYS-GLN-LEU-GLN-GLN-PHE-GLN-  
 TGG,CAA,TTG,AAT,GGG,AGG,CTT,GAA,TAC,TGC,CTC,AAG,GAC,AGG,ATG,AAC,TTT,GAC,ATC,CCT,GAG,GAG,ATT,AAG,CAG,CTG,CAG,CAG,TTT,CAG,280  
<sup>60</sup>      <sup>70</sup>      <sup>80</sup>  
 LYS-GLU-ASP-ALA-ALA-LEU-THR-ILE-TYR-GLU-MET-LEU-GLN-ASN-ILE-PHE-ARG-GLN-ASP-SER-SER-SER-THR-GLY-TRP-ASN-GLU-  
 AAG,GAG,GAC,GCC,GCA,TTG,ACC,ATC,TAT,GAG,ATG,CTC,CAG,AAC,ATC,TTT,GCT,ATT,TTT,AGA,CAA,GAT,TCA,TCT,AGC,ACT,GGC,TGG,AAT,GAG,370  
<sup>90</sup>      <sup>100</sup>      <sup>110</sup>  
 THR-ILE-VAL-GLU-ASN-LEU-ALA-ASN-VAL-TYR-HIS-GLN-ILE-ASN-HIS-LEU-LYS-THR-VAL-LEU-GLU-GLU-LYS-LEU-GLU-LYS-GLU-ASP-PHE-  
 ACT,ATT,GTT,GAG,AAC,CTC,CTG,GCT,AAT,GTC,TAT,CAT,CAG,ATA,AAC,CAT,CTG,AAG,ACA,GTC,CTG,GAA,GAA,AAA,CTG,GAG,AAA,GAT,TTT,460  
<sup>120</sup>      <sup>130</sup>      <sup>140</sup>  
 THR-ARG-GLY-LYS-LEU-MET-SER-SER-LEU-HIS-LEU-LYS-ARG-TYR-TYR-GLY-ARG-ILE-LEU-HIS-TYR-LEU-LYS-ALA-LYS-GLU-TYR-SER-HIS-CYS-  
 ACC,AGG,GGG,AAA,CTC,ATG,AGC,AGT,CTG,CAC,CTG,CAC,CTG,AAA,AGA,TAT,TAT,GGG,AGG,ATT,CTG,CAT,TAC,CTG,AAG,GCC,AAG,GAG,TAC,AGT,CAC,TGT,550  
<sup>150</sup>      <sup>160</sup>  
 ALA-TRP-THR-ILE-VAL-ARG-VAL-GLU-ILE-LEU-ARG-ASN-PHE-TYR-PHE-ILE-ASN-ARG-LEU-THR-GLY-TYR-LEU-ARG-ASN  
 GCC,TGG,ACC,ATA,ATC,CTA,AGG,AAC,TTT,TAC,TTT,CTA,AGG,AAC,CTT,ACA,GGT,TAC,CTC,CGA,AAC,TGA AGATCTCCTA GCCTG643  
 TGCCT CIGGGACTGG ACATTTGCTT CAAGCATTTCT TCAACCAGCA GATGCTGTTT AAGTGACTGA TGGCTAATGT ACTGCATATG AAAGGACACT AGAAGATTTT GAAAT 753  
 TTTTA TTAATTAATG AGTTATTTT ATTTATTTA ATTTATTTT GGAAATAAATTATTTTGG TGCAAAAGTC AAAAAAAA, ...

FIG. 4

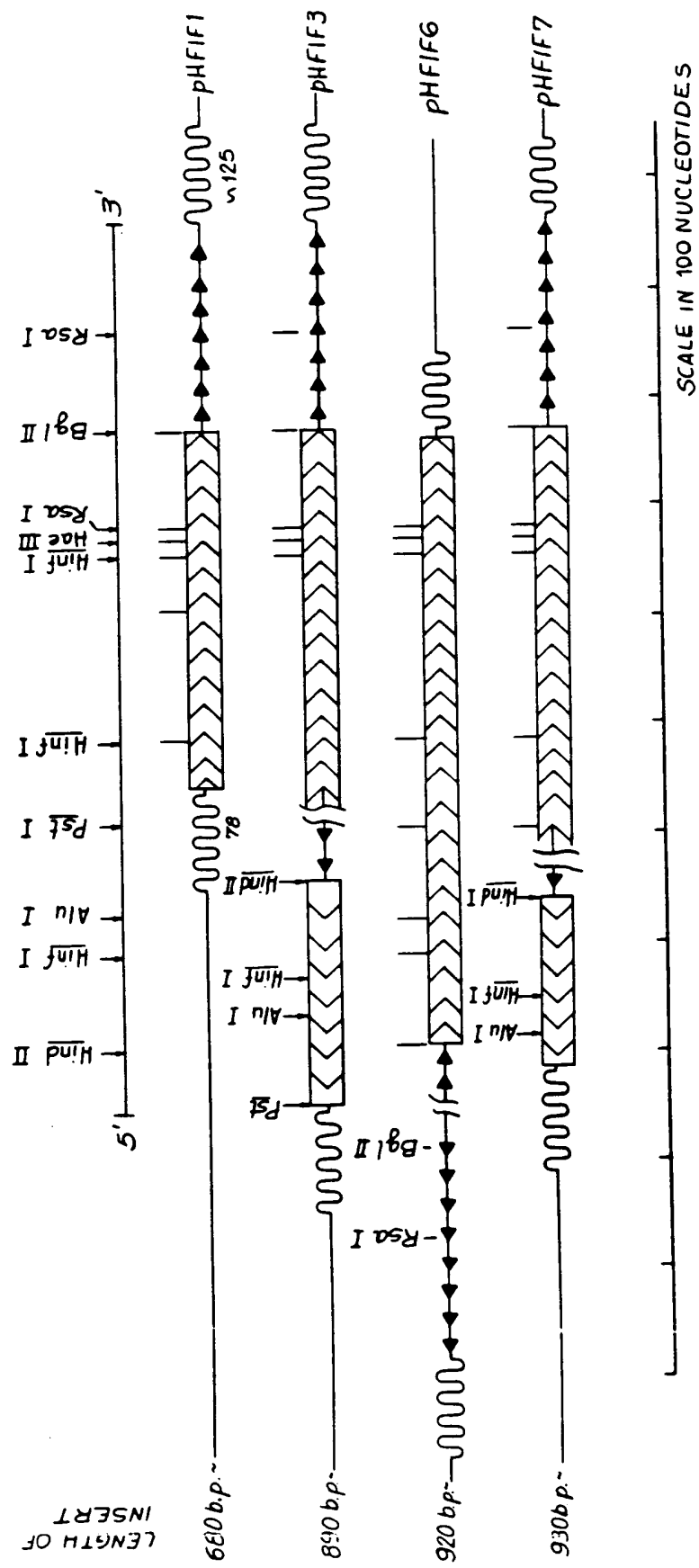


FIG. 5

# AMINO ACID COMPOSITION OF HUMAN FIBROBLAST INTERFERON

AMINO ACID	COMPOSITION		
	FROM DIRECT ANALYSIS BY TAN ET AL.	FROM DIRECT ANALYSIS BY KNIGHT ET AL.	DEDUCED FROM NUCLEOTIDE SEQUENCE
ASP	} 20.6	18.9	5
ASN			12 } 17
THR	8.0	6.8	7
SER	11.7	10.5	9
GLU	} 27.5	27.0	13
GLN			11 } 24
PRO	4.4	2.7	1
GLY	5.4	7.8	6
ALA	9.3	10.0	6
CYS	N.D.	1.7	3
VAL	7.9	6.0	5
MET	trace	2.9	4
ILE	10.0	9.0	11
LEU	26.9	20.4	24
TYR	3.2	7.5	10
PHE	7.7	9.4	9
HIS	4.6	4.9	5
LYS	12.3	11.6	11
ARG	8.6	10.9	11
TRP	0.0	1.0	3
TOTAL	168	169	166

FIG. 6



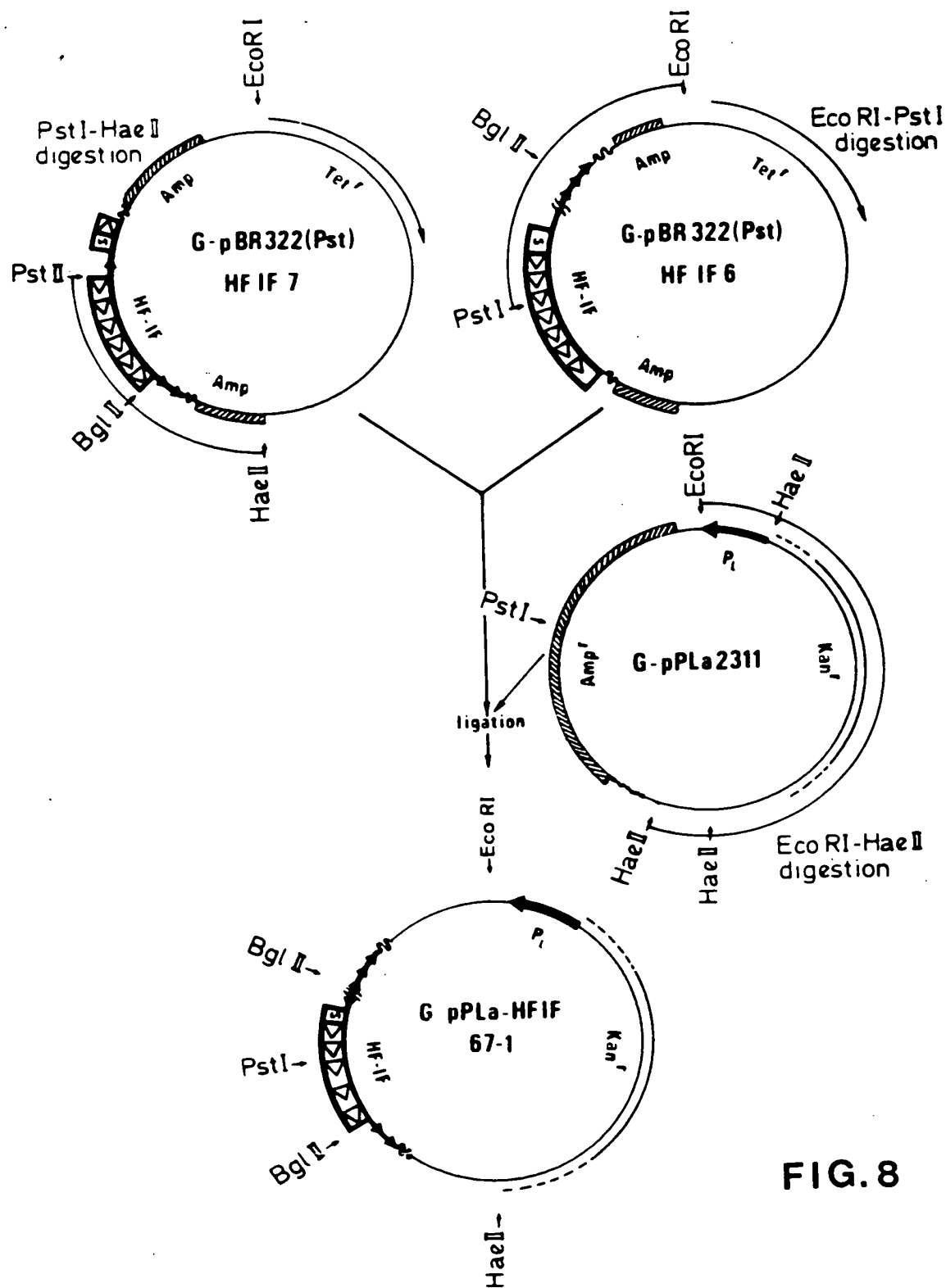


FIG. 8



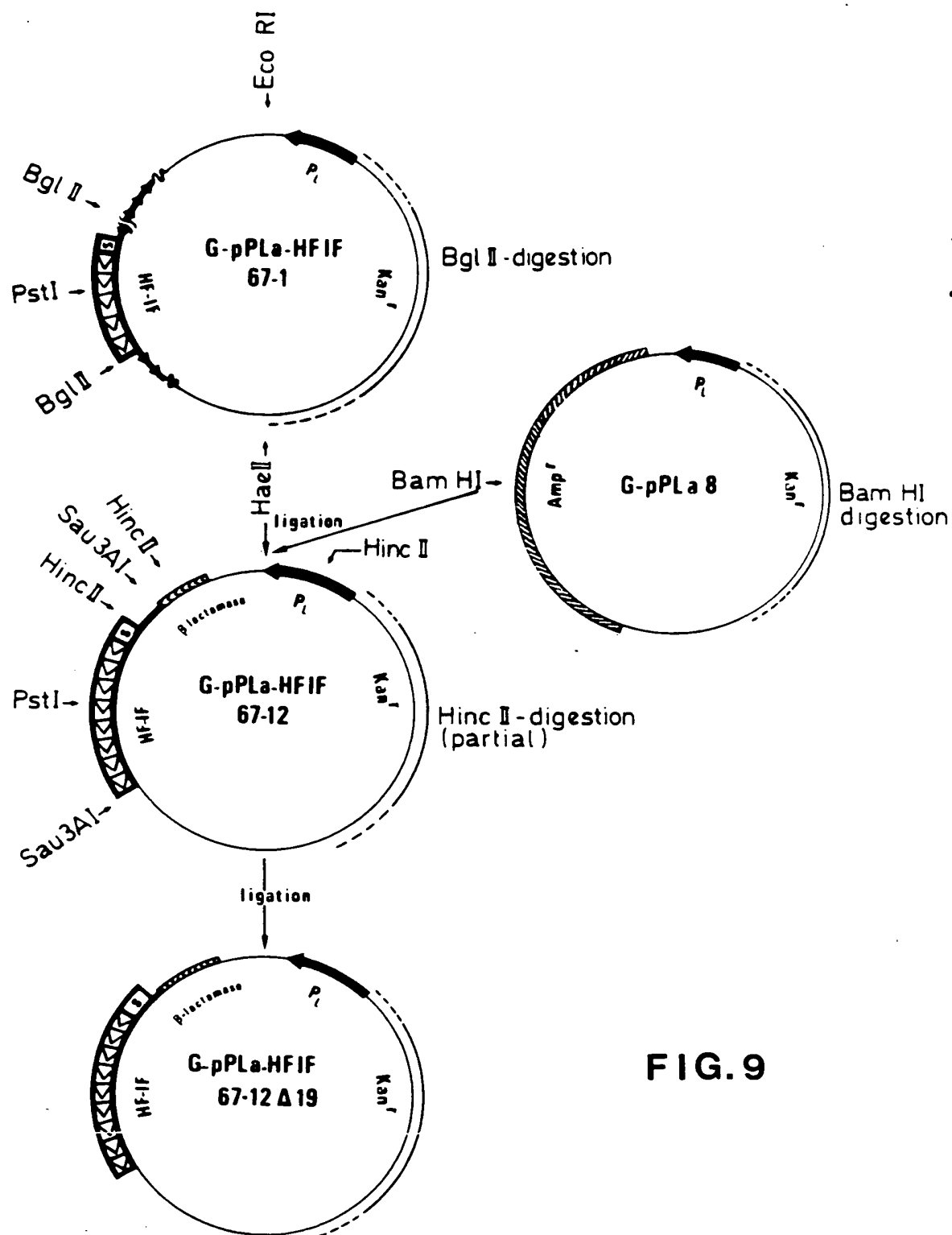


FIG. 9

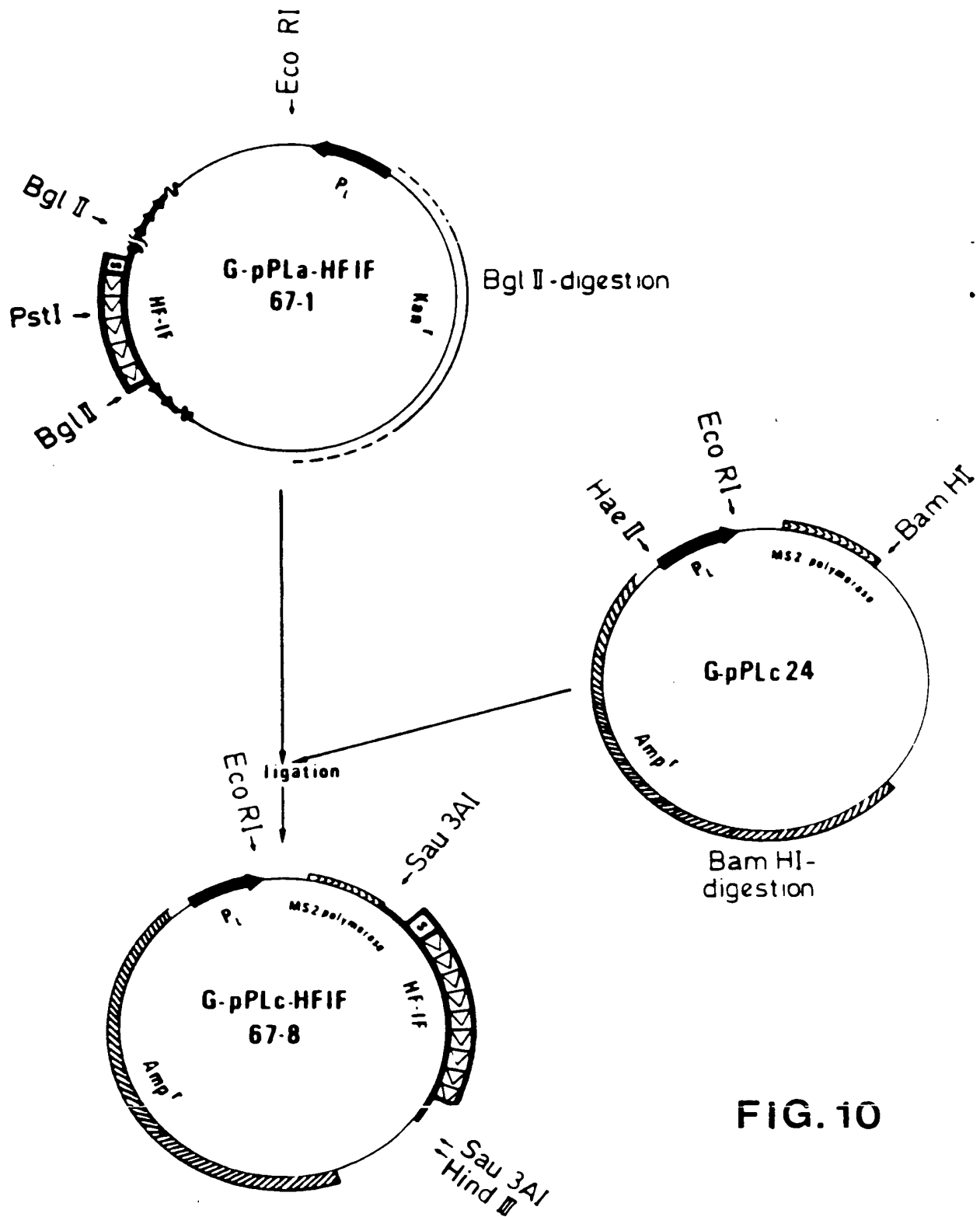


FIG. 10

FIG. 11

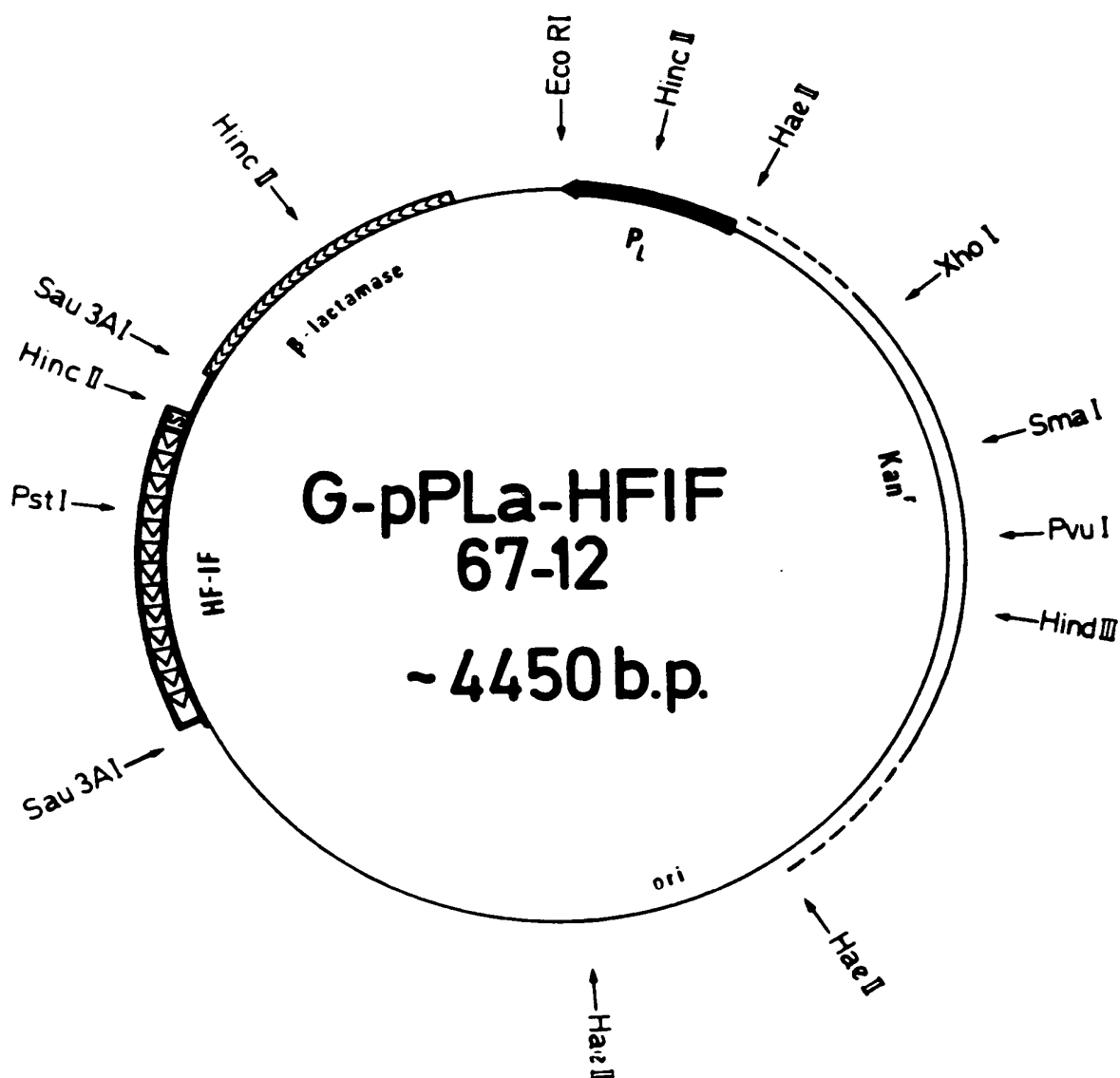


FIG.12

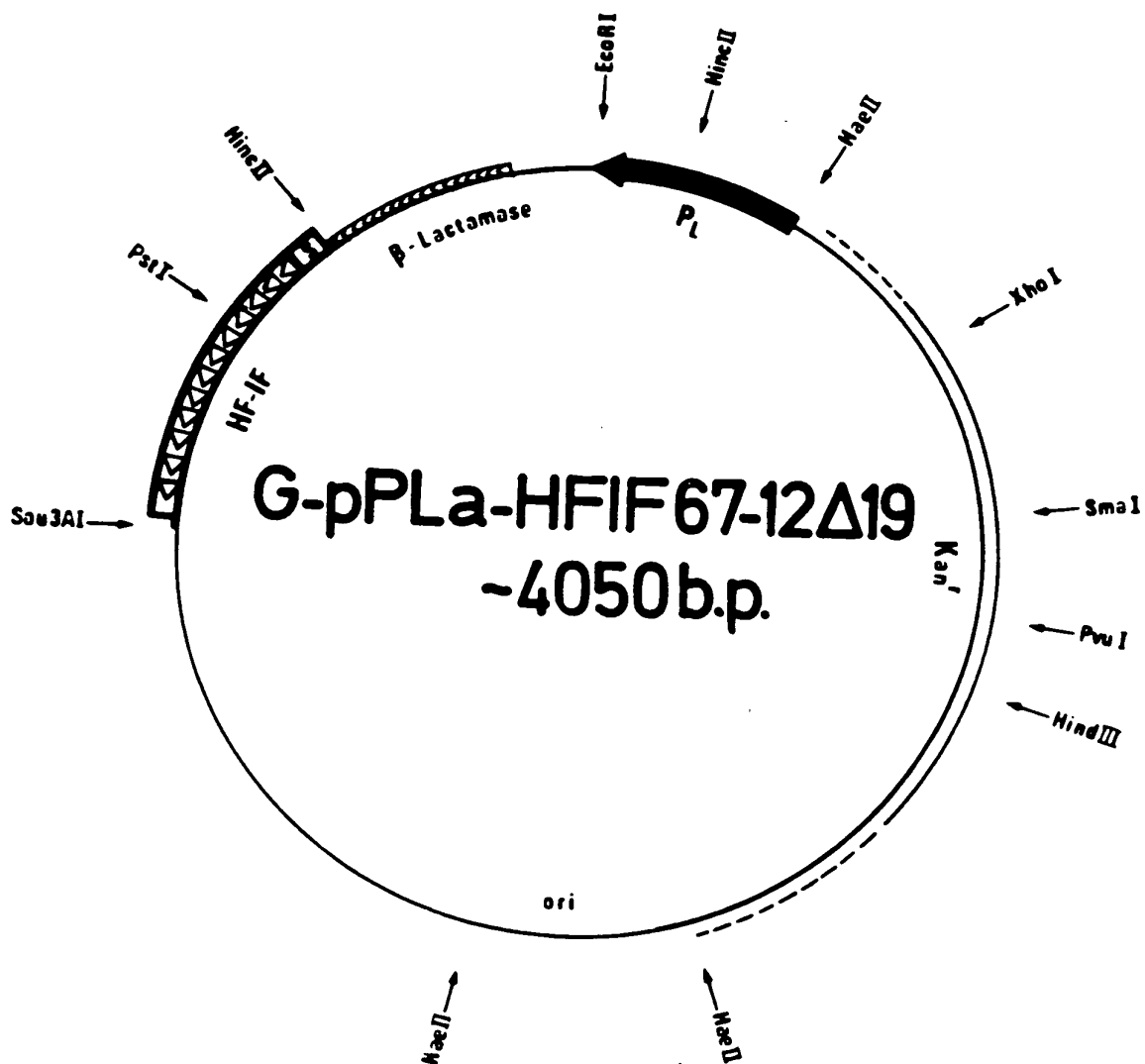


FIG.13

